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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Thu Oct 11 14:24:59 EDT 2007

Reviewer Comments:

<210> 3

<211> 720

<212> DNA

<213> Artificial sequence

<220>

<223> Engineered Aequorea-related fluorescent protein

<400> 3

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ggcgacgtaa acggccacaa gttcagcgtg tccggcgagg gcgaggggcga tgccacctac

The above <223> response mentions a protein; however, this is not a protein sequence.

<210> 6

<211> 162

<212> TYPE: PRT

<213> Artificial sequence

<220>

<223> Fragment of engineered Aequorea-related fluorescent protein
S65T, positions 68 to 229

<400> 6

Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe
1 5 10 15

Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe

Please remove the "TYPE:" heading in the above <212> response. Do not show any alphabetical headings. Also, the top amino acid line is not properly aligned with its amino acid numbers.

<210> 23
<211> 37
<212> PRT
<213> Artificial sequence
<220>
<223> His-tag amino acid sequence
<400> 23

Please provide more information in the <223> response above; please give the source of the genetic material.

Application No: 10620099 Version No: 2.0

Input Set:**Output Set:**

Started: 2007-09-20 14:58:58.525
Finished: 2007-09-20 14:59:00.108
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 583 ms
Total Warnings: 21
Total Errors: 8
No. of SeqIDs Defined: 23
Actual SeqID Count: 23

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 310	Invalid sequence type in <212> in SEQID: (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 323	Invalid/missing amino acid numbering SEQID (6) POS (2)
E 323	Invalid/missing amino acid numbering SEQID (6) at Protein (5)
E 323	Invalid/missing amino acid numbering SEQID (6) POS (6)
E 323	Invalid/missing amino acid numbering SEQID (6) at Protein (10)
E 323	Invalid/missing amino acid numbering SEQID (6) POS (11)
E 323	Invalid/missing amino acid numbering SEQID (6) at Protein (15)
E 323	Invalid/missing amino acid numbering SEQID (6) POS (16)
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W 213	Artificial or Unknown found in <213> in SEQ ID (10)
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W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
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Input Set:

Output Set:

Started: 2007-09-20 14:58:58.525
Finished: 2007-09-20 14:59:00.108
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 583 ms
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Total Errors: 8
No. of SeqIDs Defined: 23
Actual SeqID Count: 23

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22) This error has occurred more than 20 times, will not be displayed

<110> WACHTER, Rebekka M.
REMINGTON, S. James
<120> LONG WAVELENGTH ENGINEERED FLUORESCENT PROTEINS
<130> 026069-151480

<140> 10620099
<141> 2003-07-14
<150> US 09/575,847
<151> 2000-05-19
<150> US 08/974,737
<151> 1997-11-19
<150> US 08/911,825
<151> 1997-08-15
<150> US 08/706,408
<151> 1996-08-30
<150> US 60/024,050
<151> 1996-08-16
<160> 23
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<210> 1
<211> 716
<212> DNA
<213> Aequorea victoria
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gtcactactt tctcttatgg tggtaatgc tttcaagat acccagatca tatgaaacgg	240
catgactttt tcaagagtgc catgcccggaa ggttatgtac agcaaagaac tatattttc	300
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<210> 2
<211> 238
<212> PRT
<213> Aequorea victoria
<400> 2

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20	25	30	
Gly Glu Gly Asp Val Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys			
35	40	45	
Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe			
50	55	60	
Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg			
65	70	75	80
His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Gln Arg			
85	90	95	
Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val			
100	105	110	

Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile
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Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn
	130					135				140					
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly
	145					150				155		160			
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val
	165					170				175					
Gln	Leu	Ala	Asp	Tyr	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Leu	Asp	Gly	Pro
	180					185				190					
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser
	195					200				205					
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val
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Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys		
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<210>	3														
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<212>	DNA														
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<223>	Engineered Aequorea-related fluorescent protein														
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	ggcaagctga	ccctgaagtt	catctgcacc	acccggcaacg	tgccctgtgcc	ctggcccacc							180		
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	cagcaggact	tcttcaagtc	cgcattgccc	gaaggctacg	tccaggagcg	caccatcttc							300		
	ttcaaggacg	acggcaacta	caagacccgc	gccgaggtga	agttcgaggg	cgacaccctg							360		
	gtgaaccgca	tcgagctgaa	gggcatcgac	ttcaaggacg	acggcaacat	cctggggcac							420		
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	ggcatcaagg	tgaacttcaa	gatccgccc	aacatcgagg	acggcagcgt	gcagcccgcc							540		
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	tacctgagct	accagtccgc	cctgagcaaa	gaccccaacg	agaagcgcga	tcacatggtc							660		
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<210>	4															
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<212>	PRT															
<213>	Artificial sequence															
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	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe	Ile
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	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr	Thr
										50			55		60	
	Phe	Gly	Tyr	Gly	Val	Gln	Cys	Phe	Ala	Arg	Tyr	Pro	Asp	His	Met	Lys
										65			70		75	80
	Gln	Gln	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu
										85			90		95	
	Arg	Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu

100	105	110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly		
115	120	125
Ile Asp Phe Lys Asp Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr		
130	135	140
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn		
145	150	155
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser		
165	170	175
Val Gln Pro Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly		
180	185	190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu		
195	200	205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe		
210	215	220
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys		
225	230	235

<210> 5

<211> 63

<212> PRT

<213> Artificial sequence

<220>

<223> Fragment of engineered Aequorea-related fluorescent protein
S65T, positions 2 to 64

<400> 5

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Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr		
35	40	45
Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe		
50	55	60

<210> 6

<211> 162

<212> TYPE: PRT

<213> Artificial sequence

<220>

<223> Fragment of engineered Aequorea-related fluorescent protein
S65T, positions 68 to 229

<400> 6

Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Arg His Asp Phe		
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20	25	30
Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu		
35	40	45
Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys		
50	55	60
Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser		
65	70	75
His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val		
85	90	95
Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala		
100	105	110

Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu
115 120 125
Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro
130 135 140
Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala
145 150 155 160
Gly Ile

<210> 7
<211> 9
<212> PRT
<213> Artificial sequence
<220>
<223> Mutant Green Fluorescent Protein
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Cys Phe His Leu Gln Arg Trp Tyr Glx
1 5

<210> 8
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<212> PRT
<213> Artificial sequence
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<223> Mutant Green Fluorescent Protein
<400> 8
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1 5

<210> 9
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<210> 10
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Asp Glu His Lys Asn Gln
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<210> 11
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Phe Tyr His Leu

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Asp Glu His Asn Lys Gln
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<210> 18
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<223> Mutant Green Fluorescent Protein
<400> 19
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<210> 20
<211> 5
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<223> Localization sequence targeting the nucleus
<400> 20
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 1 5

<210> 21
<211> 26
<212> PRT
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<220>
<223> Localization sequence targeting mitochondrion
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 1 5 10 15
 Phe Arg Asn Ile Leu Arg Leu Gln Ser Thr
 20 25

<210> 22
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<223> Localization sequence targeting the endoplasmic reticulum
<400> 22
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<210> 23
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<223> His-tag amino acid sequence
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      1           5           10          15
      Gly Gly Gln Gln Met Gly Arg Asp Leu Tyr Asp Asp Asp Lys Asp
      20          25          30
      Pro Pro Ala Glu Phe
      35

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